

Figure 1

acgggctcgggacggaaccagctgtcaatractgcagcgtccggcgccccgcggcgacAT 60  
GGCATGGGCACTCGGGGTCACTCCTCCTGCTCGGCTCCTTACGGCGGCAGCGGGCGGCGG 120  
A W A I A V I I I P R I I T A A A A A A  
GGCGGTGACGTACGGGGTGATGTACAGTGTCTGCCATGACCTGGAGACGGTGGAGGT 130  
A V T S R G D V T V V C H D L E T V E V  
CACGTGGGGCTCGGGCCCCGACCACCACGGCGCCAACTTGAGCCTGGAGTTCCGTTATGG 240  
T W G S G P D H H G A N L S L E F R Y G  
TACTGGGGCCCTGCAACCCTGCCCGGATATTTCTGTCCGGCGCTGGTGTCACTTCGGG 300  
T G A L Q P C P R Y F L S G A G V T S G  
GTGCATCCTCCCCCGGGCGAGGGCGGGGCTGCTGGAGCTGGCACTGCGCGACGGAGGGCG 360  
C I L P A A R A G L L E L A L R D G G G  
GGCCATGGTGTTAAGGCTAGGCAGCGCGCTCCGCTGGCTGAAGCCCCGCCACCTTG 420  
A M V F K A R Q R A S A W L K P R P P W  
GAATGTGACGCTGCTCTGGACACCAGACGGGGACGTGACTGTCTCCTGGCCTGCCCACTC 480  
N V T L L W T P D G D V T V S W P A H S  
CTACCTGGGCCTGGACTACGAGGTGCAGCACCGGGAGAGCAATGACGATGAGGACGCCTG 540  
Y L G L D Y E V Q H R E S N D D E D A W  
GCAGACGACCTCAGGGCCCTGCTGTGACTTGACAGTGGGCGGGCTCGACCCCGCGCGCTG 600  
Q T T S G P C C D L T V G G L D P A R C  
CTATGACTTCCGGGTTCGGGCGTCGCCCGGGCGCGCACTATGGCCTGGAGGCGCAGCC 660  
Y D F R V R A S P R A A H Y G L E A Q P  
TAGCGAGTGGACAGCGGTGACAAGGCTTTCCGGGGCAGCATCCGCGGCCTCCTGTACCGC 720  
S E W T A V T R L S G A A S A A S C T A  
AAGCCCCGCCCATCCCCGGCCCTGGCCCCGGCCCTCCTGCCCTGGGCTGCGGCCTAGC 780  
S P A P S P A L A P P L L P L G C G L A  
AGCGCTGCTGACACTGTCCCTGCTCCTGGCGCCCTGAGGCTTCGCAGGGTGAAAGATGC 840  
A I I T I S L I I A A L R L R R V K D A  
GCTGCTGCCCTGCGTCCCTGACCCAGCGGCTCCTTCCCTGGACTCTTTGAGAAGCATCA 900  
L I P C V P D P S G S F P G L F E K H H  
CGGGAACCTCCAGGCCTGGATTGCGGACGCCCAGGCCACAGCCCCGCCAGCCAGGACCGA 960  
G N F Q A W I A D A Q A T A P P A R T E  
GGAGGAAGATGACCTCATCCACCCCAAGGCTAAGAGGGTGGAGCCCGAGGACGGCACCTC 1020  
E E D D L I H F K A E R V E P E D G T S  
CCTCTGCACCGTGCCAAGGGCACCCAGCTTGAGGCAAGGGGGCGGGAGGGGGGCCAT 1080  
L C T V P R P P S F E P R G P G G G A M  
GGTGTCACTGGGCGGGGGCACGTTTCATGGTGGGCGACAGCGGCTACATGACCTGTGAcc 1140  
V S V G G A T F M V G D S G Y M T L \*  
ttgaagtcactgcagctctataacttcaggttgaggctcacttcctgtcttttaataattca 1200  
aactcacaatacctgtgcctgtctgtatgcaaatgtgggtcaggaatattcaataaaaatg 1260  
caaatgctatgctaaaaa 1278

Figure 1

A

Delta1: MAWALAVILLPRLLTAAAAAAVTSRG 27

mγ<sub>C</sub>: MLKLLLSPRSFLVLQLLLLRAGWSSAVLMSSANEDIKADLILTSTAFEHLSAPTLP 58

Delta1: DVTVVCHDLETVEVTWCSGPDHGGANLSLEFRY---GTGALQPCPRYFLSGAGVTSGQIL 84  
+V ++E + TW S + NL+L +RY Q Q Y S +TSGQ +

mγ<sub>C</sub>: EVQCFVFNIEYMNCTWNSSEPOATNLTLYRYKVSDNNTFQESHYLFSS-KEITSGQOI 117

Delta1: PAARAGLLELALRDGGGAMVFKARQRASAWLE-----PRPPWNVTLLWTPDGDVTVSWP 138  
+ L + K ++RA L PR P N+TL + + + W

mγ<sub>C</sub>: QKEDIQLYQTFVVLQDPQ--KQRRRAVQKLNQNLVIPRAPENLTLSNLSSESQLELRWK 175

Delta1: AHSYLG--LDYEVQHRESNDELAWQTTSGPCCDLTVGGDLPARCYDFRVRASPRAAHYG 196  
+ L Y VQ+R SN D + ++ +D + Y FRVR+ G

mγ<sub>C</sub>: SKHIKERCLQYLQYR- SNRDRSWTELIVNHEPRFSLPSVDELKRYTFEVRSRYNPI-CG 233

Delta1: LEAQPSEWIAVTRLGAASAASCTASPAPSPALA 230  
Q S+W+

mγ<sub>C</sub>: SSQQWSKWSQPVHWGSHTVEEN 255

B

Delta1	LLPCVPDPSCGSFPGLEKHHGNFQAWIA (19AA)	PKAKRVEPEDGTSIDCT
	: * : * * * * * * * * * * :	: *
mEPOR	IWPGIPSPSEFEGLFTTHKGNFQLWLL (16AA)	DPPAHLEVLSEPRWAV
	* : * * * * * * * * * * :	* : * * * *
mIL-2RB	LKCHIPDPSEFFSQLSSQHGGDLQKWLS (14AA)	PEISPLEVLDGDSKAV
	: * * * * * * *	: * * *
mgp130	IWPNVDPSPKSHIAQ-----WSP (20AA)	TDVSVVEIEANNKPC
	: * * * * *	: * * :
AIC2B	WKEKIPNPSKSLLFQDGKGL----WPP (34AA)	NNVSPLTIEDPNIRV

Box1 region      Conserved tryptophan      Box1 region

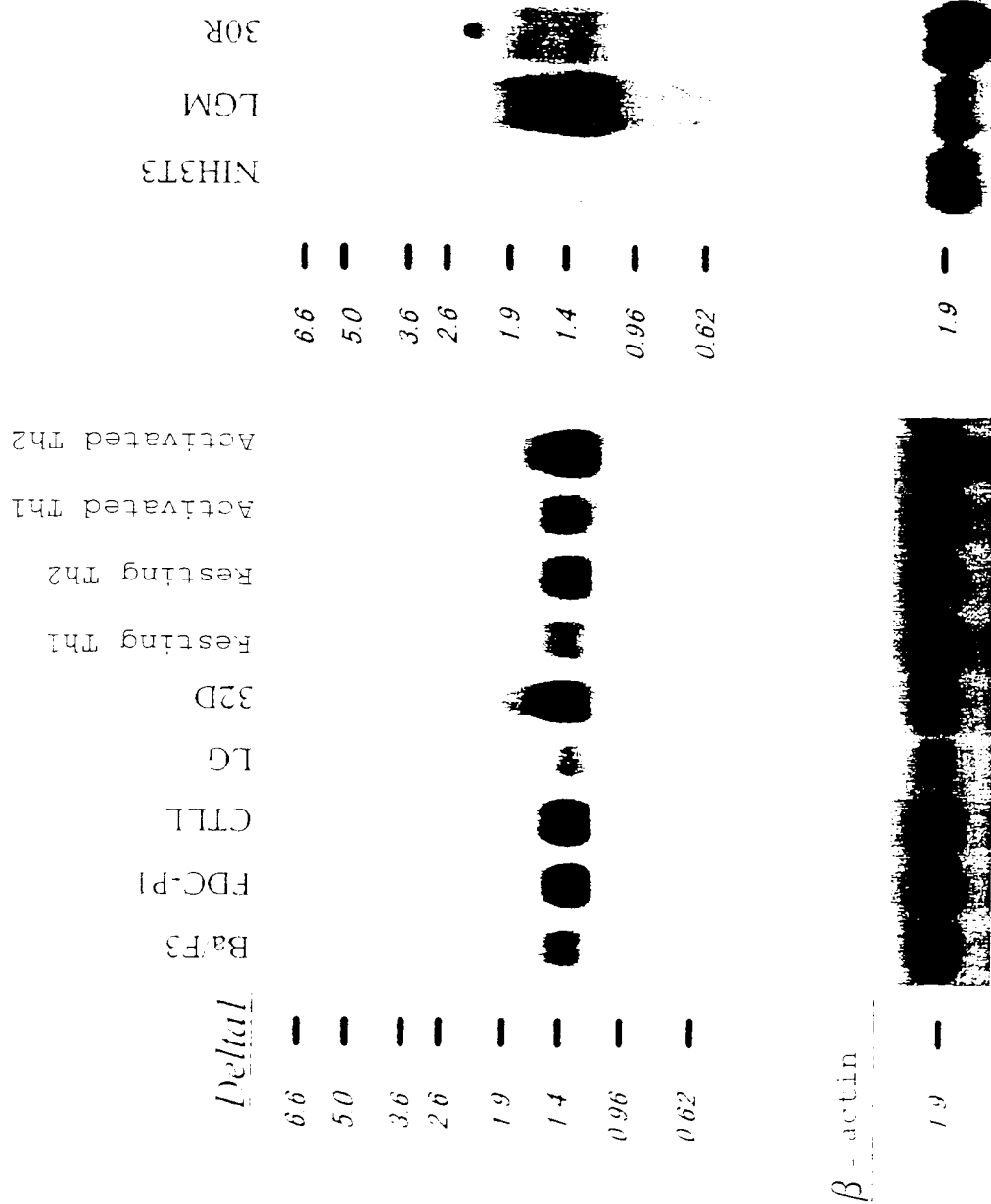


Figure 3

Heart  
 Brain  
 Spleen  
 Lung  
 Liver  
 Skeletal muscle  
 Kidney  
 Testis

*Delta*

9.5  
 7.5  
 4.4  
 2.4  
 1.35



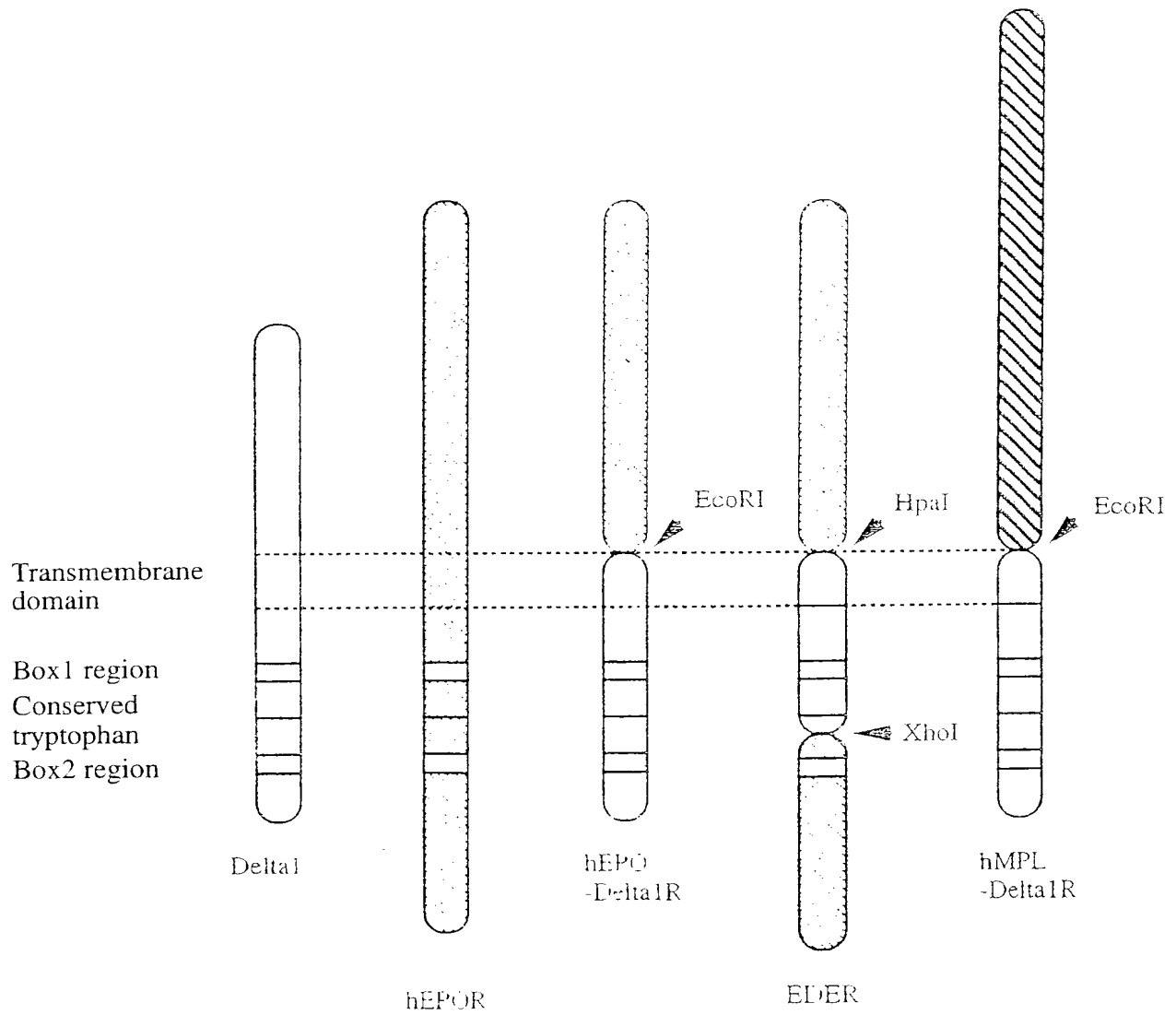
$\beta$ -actin

2.4  
 1.35



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Figure 5



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Figure 6

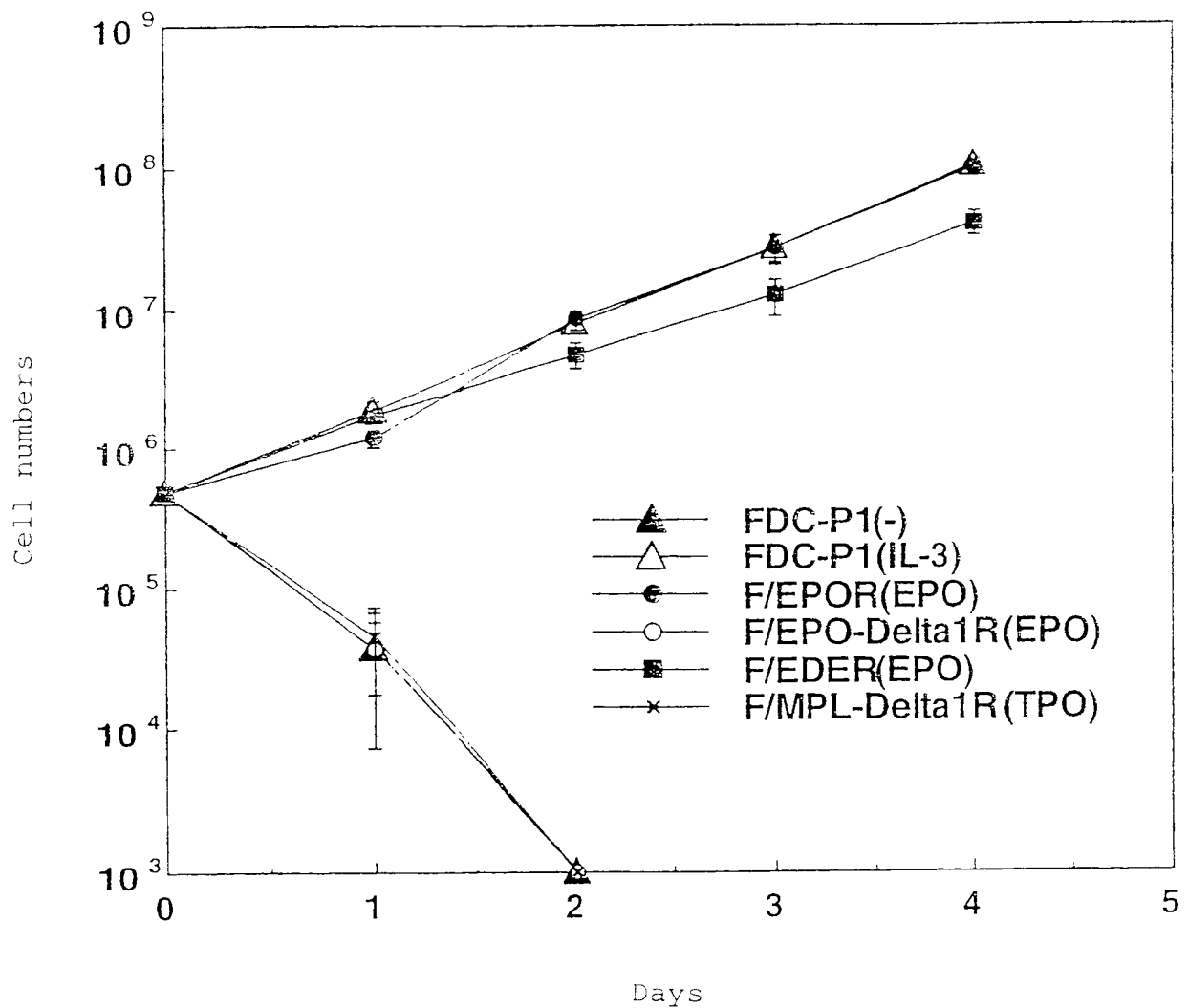


Figure 1

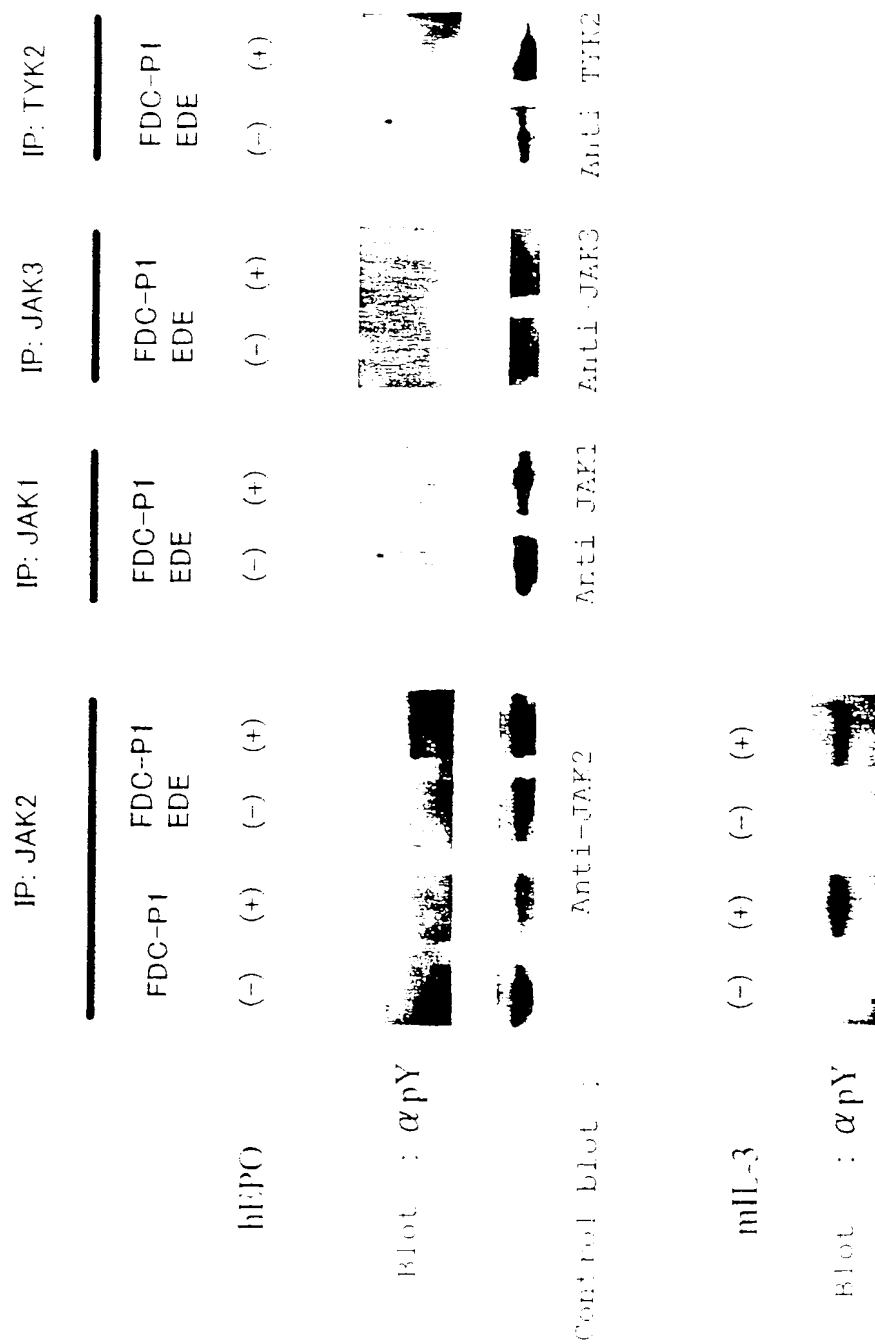
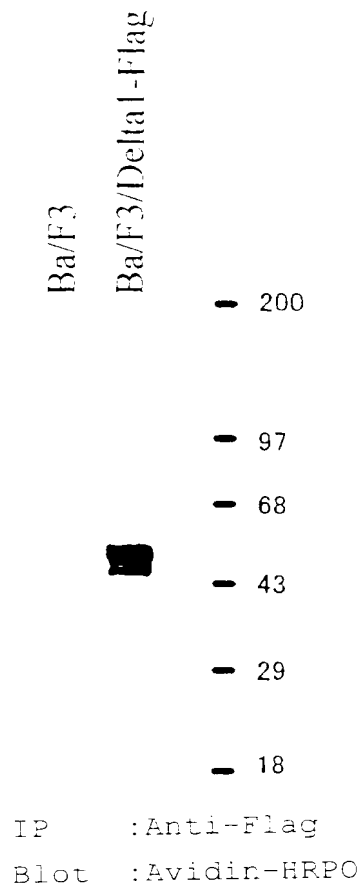


Figure 8



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9.9

Figure 9

